

Figure 1

SEQ ID NO:21	(gi 1709203)	1	MARNGSLEEFGLVAVDAAKRAGEIIRKGFHETKHVVHKGQVDLVTTETDKACEDLIFNHLK	60
SEQ ID NO:22	(gi 1709205)		MAQNGSVEQFLDVAVEAAKKAGEIIREGFYKTKHVEHKGMDLVTTETDKACEDLIFNHLK	
SEQ ID NO:2			MAE-----EQFLAVAVDAAKNAGEIIRKGFYQTKNVEHKGQVDLVTTETDKACEDLIFNHLR	
SEQ ID NO:4			MVDNDSLSEFLASAVDAAQKAGEIIRKGFYQTKNVEHKGQVDLVTTETDKACEELIFNHLK	
SEQ ID NO:6			MAE-----EQFLAAAVGAAKSAGEIIRKSFYLSKKVEHKGQVDLVTTETDKACEDLIFNHLR	
SEQ ID NO:8				
SEQ ID NO:21	(gi 1709203)	61	QHFPCHKFIGEETSAAT-GDFDLTDEPTWIIVDPVDGTTNFVHGFPFVCSIGLTIGKIPT	120
SEQ ID NO:22	(gi 1709205)		QRFPCHKFIGEETAA-CGNFELTDEPTWIIVDPLDGTTFVHGFPFVCSIGLTIEKKPT	
SEQ ID NO:2			KHYPDHKFIGEETSAGLGATADLTDDPTWIIVDPLDGTTFVHGFPFVCSIGLTIVGK----	
SEQ ID NO:4			QLYPCHKFIGEETAA-YGTTELTDPTWIIVDPLDGTTFVHGFPFVCSIGLTIGKTPT	
SEQ ID NO:6			MLYPDHKFIGEETSAALGSTDDLTIDPTWIIVDPLDGTTFVHGFPFVCSIGLTIGKIPT	
SEQ ID NO:8				
SEQ ID NO:21	(gi 1709203)	121	VGVVYDPIIDELFTGINGKGAYLNGKPIKVSSQSSELVKSLLGTEVGTTRDNLTVETTTRR	180
SEQ ID NO:22	(gi 1709205)		VGVVYNPIIDELFTGIDGKGAFLNGKPIKVSSQSSELVKSLLGTEVGTTRDNLTVETTTRR	
SEQ ID NO:2			IGVVYNPIINELFTGIHGKGAFLNGNPIKVSSQSSELVKSLLGTEVGTTRDNLTVETTTRR	
SEQ ID NO:4			VGVVYNPIMNELFTAVRGKGAFLNGSPIKTSPQNELVKALMVTEVGTTRDNLTVETTTRR	
SEQ ID NO:6				
SEQ ID NO:8				
SEQ ID NO:21	(gi 1709203)	181	INNLLFKVRSRLMCGSCALDLCWVACGRLELFYLYGGPVDVAGGAVIVKEAGGVLFDP	240
SEQ ID NO:22	(gi 1709205)		INSLLFKVRSLMCGSCALNLCGVACGRDLDFELEGGPWDVAGGAVIVKEAGGVFDP	
SEQ ID NO:2			-----VLRGAGLS-----	
SEQ ID NO:4			-----IACGRLDVFFELGFGGPWDVAGGAVIVREAGGVFDP	
SEQ ID NO:6			INKLLFKIRSIRMGSLALNMCGVACGRDLDCYEIGFGGPWDVAAAGALILKEAGGVFDP	
SEQ ID NO:8				
SEQ ID NO:21	(gi 1709203)	241	SGSEFDITSQRVAATNPHLKEAFVEA---LQLSEYVS	277
SEQ ID NO:22	(gi 1709205)		SGSEFDLTARRVAATNAHLKDAFIKA---LNE---	
SEQ ID NO:2			-----I-----	
SEQ ID NO:4			-----T-----	
SEQ ID NO:6			SGADFAITSQRVAVSNPFKDELVEPTRRKMGEIYN.	
SEQ ID NO:8			SGDEFDLMAQRMAGSNGHLKDQFIKA---LGDAS.---	

181 240
 SEQ ID NO:23 (gi 3915048) PVSCVSI GLLIQDIPTVGVVYNPFRQELFRAATSLGATLNR-----RPIQVSTTASLDK
 SEQ ID NO:24 (gi 1652942) PIFATLIGLVDADMRPVLGIAHQPISGDRWQGVQGEQSNVNGIP-LVNPYKASEINLTAA
 SEQ ID NO:10 PSFSVSI GVL YRGKPAAATVVEFCG GPMCWSTRTISASSGKAYCNGQKIHVSPTEKVEQ
 SEQ ID NO:12 -----MCWTTTRTIFPFAGGAYYIGQRIHVQSOTDKVEQ
 SEQ ID NO:14 PLFGTLIAL LHNG-KPVI GVIDQPI LRERWIGVDGKQTTLNGQE-I--SVRSCNL-LAQA
 SEQ ID NO:16 -----LTKVEQ
 SEQ ID NO:18 PVFGTLVALLQNG-TPILGIIDQPVLRERWIGIAGKRTSLNGQE-I--STRTCAD-LSQA
 SEQ ID NO:20 PLFGTLIAL LHNG-KPVMGIIDQPI LRERWVGVDGKKTTLNGQE-I--SVRPCNV-LEQA

241 300
 SEQ ID NO:23 (gi 3915048) SLLVTG---FAYDRVKTLDN NYPEFCYLTHLTQGVRRSGSAAIDLIDVACGRLDGYWERG
 SEQ ID NO:24 (gi 1652942) CIVSTTPLMFTTPVQQQKMADIYRQCORTAFGGDCFNYSAAAGWTAMPLVIVEA----D
 SEQ ID NO:10 SLLVTG---FGYEHDDAWLTNINLFKEFTDVS RGVRRGLSAAADMSHVGLGITEAYWEYR
 SEQ ID NO:12 SLLVTGFGYEHDDAWTTNMNLFKEFTDISRGVRR--LGSAAADMSHIGL GITE--AYWE
 SEQ ID NO:14 YLYTTSPLHFEADAEDA-FIRVRNKVKVPLYGCD CYAYALLASGFVDI---VVES-----G
 SEQ ID NO:16 SLLVTG---FGYEHDDAWVTNINLFKEYTDISRGVRRGLSAAADMSHVALGITEAYWEYR
 SEQ ID NO:18 YLYTTSPLHFN GDAEEA-FIRVRSKVKFQLYGCDCYAYALLSSGFVDL---VVES-----G
 SEQ ID NO:20 YLYTTSPLHFE GDAEDA-FIRVRDKVKVPLYGCD CYAYALLASGFVDL---VVES-----G

301 360
 SEQ ID NO:23 (gi 3915048) INPWDMAAGIVIVREAGGIVSAYDCSPLDLSTGRILATNGKIHQELSQALAAPQ-----
 SEQ ID NO:24 (gi 1652942) LNFYDFCALIPI LTGAN YCFTDWQKEL-----TPESTE VVASPNPKLHSE
 SEQ ID NO:10 LKPWDMAGVLIVEEAGGVVTRMDGGEFTVFD RSVLVSNGVVHDQLLERIRPATEDLKKK
 SEQ ID NO:12 YRLKPWDVHAGVLIVEEAGGVVTRMDGGEFTV FDRSVLVSNGLVHGQV-----
 SEQ ID NO:14 LKPYDFLSLVPVIEGAGGSITDWRGDKLH-----WPVTAESRPTSFNVVAAAGDARVHKE
 SEQ ID NO:16 LKPWDMAGVLIVEEAGGMVSRMDGGEFTVFD RSVLVSNGVVHDQLLDRIGPATEDLKKK
 SEQ ID NO:18 LKPYDFLALIPVIEGAGGVITDWKGD KLF-----WEASPLSIATSFNVVAAAGDKQIHQQ
 SEQ ID NO:20 LKPYDFLSLVPVIEGAGGSITDWEGNKLH-----WPVSSES RPTSFNVVAAAGDSHVHGQ

361 381
 SEQ ID NO:23 (gi 3915048) -----WF--QQYAAARAQKI
 SEQ ID NO:24 (gi 1652942) ILAFL---Q-----
 SEQ ID NO:10 GIDFSLWFKPKYPT---DF.
 SEQ ID NO:12 -----CL
 SEQ ID NO:14 ALDALRWR.-----
 SEQ ID NO:16 GIDFSLWFKPKYPT---DF.
 SEQ ID NO:18 ALDSLQWK.-----
 SEQ ID NO:20 ALAALRWR.-----